| | | 1/7 | · | | |
|----------------------------------|--|--|---|--|--------------------------|
| mkrm1 hkrm1 mkrm2 hkrm2 | ATGGGGACAC ATGGGGACAC | T G G G G G G G G G G G G G G G G G G G | GGCTTCCTC | CTCGCGCT CTCGCGCT CTCCTCT | 29 29 37 40 |
| mkrm1 | GCTCTCGGCC | GCTGCGCTCA | CTCTGG | C G G C C C G G C C | 65 |
| hkrm1 | GCTCTCGGCC | GCGGCGGTCA | CGCTGG | C G G C C C G G C C | 65 |
| mkrm2 | TCCCATTGCT | GCTGCGGCTG | CACGGGGCCT | C A G C A G G G A G | 77 |
| hkrm2 | TCCTCCGCT | GCTGCAGCCG | CGTGGGGCCT | C G G C T G G G A G | 80 |
| mkrml hkrml mkrm2 hkrm2 | TO COOCTO | CCCCCTCC CCCCCTCC CCACCTTC. | GCCCCGAGTG GCCCCGAGTG . TCCGAATG | CTTCACAGCC TTTCACAGCC CTTCCAGGTG CTTCCAGGTG | 105 105 114 117 |
| mkrm1 hkrm1 mkrm2 hkrm2 | A A C G G G C A G A A D G G D G C T G A A C G G G C T G A A C G G G C T G | ATTACAGGGGATTATACAGGGGATACCGAGGAGGAGGAGGAGGGAG | AACACAGAGC AACACAGAAC CCAGCAGAAC CCAGCAGAAC | TGGACAGCAC TGGACAGCAC TAGACCGGCC | 145 145 154 157 |
| mkrm1 hkrm1 mkrm2 hkrm2 | T G C A . A G G T A C A . A G G C A C G G G G G G C C G C G G G G C | TGGGAAGCCA GGGGAAGCCA TGGACGCCT GGGCCG | TGTCTGTTGT TGTCTTTTT TGTCTTTTTGT | G G A A C G A G A C G G A A C G A G A C G G G A C C A G A C G G G A C O A G A C | 182 182 194 197 |
| mkrm1 | TTTCCAGCAT | C C G T A C A A C A | CGCTGAAGTA | C C C C A A C G G G C C C C C A A C G G C C C C | 222 |
| hkrm1 | TTTCCAGCAT | C C A T A C A A C A | CTCTGAAATA | | 222 |
| mkrm2 | ACAGCAGCAC | A G C T A C A G C A | CCGCCAGCGA | | 234 |
| hkrm2 | GCAGCAACAC | A G C T A C A G C A | GCGCCAGCGA | | 237 |
| mkrm1 | G A A G G A G G A C | TGGGGGAGCA | CAACTATTGC | A G A A A T C C A G | 262 |
| hkrm1 | G A G G G G C C | TGGGTGAGCA | CAACTATTGC | A G A A A T C C A G | 262 |
| mkrm2 | C G C T G G G G T | TGGGTGCGCA | TAACTTCTGT | A G G A A C C C A G | 274 |
| hkrm2 | C G C T G G G G C | TGGGGGCA | CAACTTCTGC | C G T A A C C C A G | 277 |
| mkrm1 | ATGGAGAGGT | GAGCCCTTGG | T G C T A C G T G G | C C G A G C A T G A C A G A G C A C G A C A G A G A C A G A C T G A G A C A G A | 3.02 |
| hkrm1 | ATGGAGAGGT | GAGCCCGTGG | T G C T A T G T G G | | 302 |
| mkrm2 | ACGGTGATGT | GCAGCCGTGG | T G C T A C G T G G | | 314 |
| hkrm3 | ACGGTGACGT | GCAGCCGTGG | T G C T A C G T G G | | 317 |
| mkrm1 | GGACGGAGTC | TACTGGAAGT | ACTGTGAMAT | TCCTGCCTGC | 342 |
| hkrm1 | GGATGGTGTC | TACTGGAAGT | ACTGTGAGAT | ACCTGCTTGC | 342 |
| mkrm2 | AGAGGGCÄTC | TACTGGGGGT | ACTGTGATAT | CCCCACATGT | 354 |
| hkrm2 | GGACGCATC | TACTGGCGCT | ACTGCGACAT | CCCCTCCTGT | 357 |
| mkrm1 | CAGATGCCTG | GAAACCTTGG | CTGCTACAAG | GATCATGGAA | 382 |
| hkrm1 | CAGATGCCTG | GAAACCTTGG | CTGCTACAAG | GATCATGGAA | 382 |
| mkrm2 | CAGATGCCTG | GGTACCTGGG | CTGCTTCGTG | GACTCTGGGG | 394 |
| hkrm2 | CAGATGCCAG | GCTACCTGGG | ATGCTTTGTG | GACTCAGGGG | 397 |
| mkrml hkrml mkrm2 hkrm2 | | T C T C A C G G G C T C T A A C T G G C T C T C A G T G G T C T C A G C G G C | A C C A G T A A A A A C C A G T A A A A C C A G T G G C A C C C G C C A | CCTCTAACAA CGTCCAACAA CCTCCACAAA CCTCCACAAA | 422 422 434 437 |
| mkrml | G C T C A C C A T A | CAAACTTGTA | TCAGCTTCTGTGTCAGTTTTTGTTGTTGTTGTTGTTGTTGTTGTTG | T C G G A G T C A G | 462 |
| hkrml | A C T C A C C A T A | CAAACTTGCA | | T C G G A G T C A G | 462 |
| mkrm2 | G C T C A C T G T C | CAAGTGTGCC | | C C G C A T G A A G | 474 |
| hkrm2 | G C T C A C G G T C | CAGGTGTGCC | | C C G C A T G A A G | 477 |
| mkrml | AGATTCKAGT | TTGCTGGGAT | C G A G T C A G G C G A G T C A G C T C A G C T G G T G G T G G T G G C T G G T G G A G G C T G G C T G G C G T G G C T G G C G T G C G C | TATGCCTGCT | 502 |
| hkrml | AGGTTCKAGT | TTGCTGGGAT | | TATGCTTGCT | 502 |
| mkrm2 | GGCTACCAGC | TGGCTGGTGT | | TATGCCTGCT | 514 |
| hkrm2 | GGTACCAGC | TGGCGGGCGT | | TAGGCCTGCT | 517 |
| mkrml | TCTGTGGAAA | C A A T C C T G A C | T A C T G G A A G C T A C T G G A A G T C T G G C C G C G C T O G C C C G G | ACGGGGAGGC | 542 |
| hkrml | TCTGTGGAAA | C A A T C C T G A T | | ACGGGGAGGC | 542 |
| mkrm2 | TCTGTGGCTC | T G A A A G T G A C | | GACGTCCAGC | 554 |
| hkrm2 | TCTGTGGCTC | T G A A A G C G A C | | GACGCCTGGC | 557 |
| mkrm1 | G G C C A G C A C C | GAGTGCAATA | GTGTCTGCTT | C G G G G A C C A C | 582 |
| hkrm1 | A G C C A G T A C C | GAATGCAACA | GCGTCTGCTT | C G G G G A T C A C | 582 |
| mkrm2 | C C C T G C C A C C | GACTGTGACC | AGATCTGTTT | T G G C C A C C C A | 594 |
| hkrm2 | C C C C G C C A C C | GAGTGTGACC | AGATCTGTTT | C G G C C A C C C T | 597 |

Multiple-alignment of mouse and human kremen DNAs (3-1)

Fig. 1 a

| | 4.0 | 2/7 | | | |
|----------------------------------|---|--|--|--|------------------------------|
| mkrm1 hkrm1 mkrm2 hkrm2 | T | G G G G G G A G G G G A G G G G G G G G | TTABBACEBD TKEBARCEBT ATDABCACTA BTDBBBBBT | ATCCTCTTTG ATCCTCTTTG GGCATCTATG GGCGTCTATG | 622 622 634 637 |
| mkrm1 | AÇAÇTCTĞĞT | G G C G C C T G C | G C T G G C A A C T | ACTCAGCCAT | 662 |
| hkrm1 | ACACTCTĞĞT | G G G C G C C T G C | G C T G G C A A C T | ACTCAGCCAT | 662 |
| mkrm2 | AAĞTĞTCTĞT | G G G C T C C T G C | C A G G G A A A C T | GGTCGGCTCC | 674 |
| hkrm2 | AAĞTĞTCĞĞT | G G G C T C C T G C | C A G G G G A A C T | GGACAGCCCC | 677 |
| mkrm1 hkrm1 mkrm2 hkrm2 | GGCAGCCGTG GTCTTCTGTG TCAAGGAGTC TCAGGGCGTC | GTGTACTCCC GTGTATTCCC ATGTAGTCCC ATGTACTCCC | CTGACTTCCCCCGGACTTCCCC | TGACACCTALC GGAGACCTAT GGATGAGTAT GGACGAGTAC | 702 702 714 717 |
| mkrm1 | A C C A C C A C C A C C A C C A C C A G A C C A G A C C C A G A C C C C | GAGTCTGCTA | CTGGACCATC | CGBGTTCCAG | 742 |
| hkrm1 | | GGGTCTGCTA | CTGGACCATC | CGGGTTCCGG | 742 |
| mkrm2 | | GGAACTGCAG | CTGGGTATTG | GGCCAACTGG | 754 |
| hkrm2 | | GGAACTGCAG | CTGGCCCT | GGCCCAGCAG | 757 |
| mkrm1 hkrm1 mkrm2 hkrm2 | GAGCCTCTCG GAGCCTCCCA GGGCTGTGC. GGGCCGGGG. | CATCCATTTCCATTCCATCCATCCATCCATCCACTCCACTCCACTCCACTCCACTCCACTCCACCTCACCTACCTCACCAC | AACTTCACCC AGCTTCCCCC ACCTTCCCCC ACCTTCCCCC | TGTTTGATAT TATTTGACAT TCTTTGGAGTT TCTTTGGAGCT | 782 782 791 794 |
| mkrm1 hkrm1 mkrm2 hkrm2 | TOTOAGDOACT CACAGOACTC CACAGOATTCT CACAGOACTCA | OCACACADO BOTACADOS DOCACACACA DOCACACACACACACACACACACACACACACACACACACA | T G G A G C T G C T T G G A G C T T C T T G G A G C T A C G T G G A G C T G C G | GGACGCTAC GGACGCTAC GGACGTCT | 822 822 829 832 |
| mkrml | ACCCACCGCG | TCCTGGTCCG TCCTAGCCCG ACCTACTCCG GCCTGCTCCG | G C T C A G T G G G | A G G A G C C G C C | 862 |
| hkrml | ACCCACCGTG | | C T T C C A C G G G | A G G A G C C G C C | 862 |
| mkrm2 | ACCCACCGCA | | T G C C T T C G A C | G G C G C C C A T C | 868 |
| hkrm2 | CGTCCGGCA | | C G C T T C G A T | G G C G C C C G C C | 871 |
| mkrm1 hkrm1 mkrm2 hkrm2 | CGCCTCTGTC CACCECTCTC CGCCGCCTCC | TTTCAATGTC CTTCAACGTC GGGACCGCTG CGGGCCGCTG | TCTCTGGATT TCTCTGGACT CGCCTGCGCA CGGCTGGGCA | TTGTCATTTT TCGTCATCTT CTGCTCCGCT CTGCCGCGT | 902 902 908 911 |
| mkrm1 | GTATTTCTTC | TCTGATCGCA | TCAATCAGGC | CCAGGGATTT | 942 |
| hkrm1 | GTATTTCTTC | TCTGATCGCA | TCAATCAGGC | CCAGGGATTT | 942 |
| mkrm2 | GCTGCTCACC | TTCCGCAGCG | ACGCAAGAGG | CCATGCTC | 946 |
| hkrm2 | GCTGCTCACC | TTCCGAAGC | ACGCCCCGG | CCACGCGC | 949 |
| mkrm1 | GCTGTGTTGT | ACCAAGCCAC | CAAGGAGGAA | C C G C A C A G G | 982 |
| hkrm1 | GCTGTTTTAT | ACCAAGCCGT | CAAGGAAGAA | C T G C C A C A G G | 982 |
| mkrm2 | AAGGCTTCGC | GCTCACCTAC | CGCGGGCTGC | A G G A T A C A G T | 986 |
| hkrm2 | AAGGCTTCGC | GCTCACCTAC | CGCGGCTGC | A G G A C G C C C | 989 |
| mkrm1 | AGAGACCTGC | T G T C A A C C A G | ACCCTOOCAG | A G G T G A T C A C | 1022 |
| hkrm1 | AGAGGCCCCC | T G T C A A C C A G | ACGCTGGCCG | A G G T G A T C A C | 1022 |
| mkrm2 | GGAGGGCAGA | G C A T C T C C A G | AGGATT.CAA | C T G A G A G T C T | 1025 |
| hkrm2 | TGAGGACCCA | G A G G C C C C G | AGGCCT.CGG | C C C A G A C C C C | 1028 |
| mkrm1 | CGAGCAAGCC | AACCTCAGTG | T C A G C G C T G C | 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 | 1062 |
| hkrm1 | GGAGCAGGCC | AACCTCAGTG | T C A G C G C T G C | | 1062 |
| mkrm2 | CGCAGGGAC | CGCGATGGGG | C T A A C G C G A G | | 1065 |
| hkrm2 | CGCGGCGCC | CTCGACGG | C C A A C G T G A G | | 1068 |
| mkrm1 hkrm1 mkrm2 hkrm2 | AAAGTCCTCT AAAGTCCTCT AAGCCC | ATGTCATCAC ATGTCATCAC GGAGCTGCAC GGGGCTCCGC | CCCAGCCCC CACCAGCCCC AGGCTTCGAT AGGCTCGAT | A G C C A C C C T C A G C C A C C C A C A G G T G C C C A A T G G G G C C G G | 1102 1102 1101 1104 |
| mkrm1 | C G C A G A C T G C | CCCAGGTAGC | CATTCCTCTCCCCCCCCCCCCCCCCCCCCCCCCCCCCC | CACCGTCAGT | 1142 |
| hkrm1 | C T C A G A C T G T | CCCAGGTAGC | | CGCCACCAT | 1142 |
| mkrm2 | G T C T T C T C C A | CCGTGACGGC | | CTGCTGCTGT | 1141 |
| hkrm2 | G T C T T C T C G A | CGGTGACGGC | | CTGCTGCTGC | 1144 |
| mkrml | TGGGGCCAAC | A G C C A C A G A G | T G G A A G G A T O T T G A A G G A T G T T G C T G C G T C C G C C C C C C C C C C C | GACTGTGTAC | 1182 |
| hkrml | GGGGGCTGGA | A G C C A C A G A G | | GACAGTCTAT | 1182 |
| mkrm2 | TGCTCCTGTC | C C T A C T G C G T | | GACGG | 1176 |
| hkrm2 | TGCTCCTGG | G C T G C T G C G T | | GACGGTGCGG | 1184 |

Multiple-alignment of mouse and human kremen DNAs (3-2)

Fig. 1 b

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| mkrm1 hkrm2 mkrm2 hkrm2 | GGCCTGGCGA GGTCTGGCAA GGCGCTGGGG | CCCTCCTCAT CTCTCCTCAT CAGGGCCTGA | CCTCACAGTC CCTCACAGTC | ACAGCAGTTG 1222 ACAGCCATTG 1222 AGCTG 1181 GGTGGAGCTG 1223 |
|----------------------------------|---|--|--------------------------------|---|
| mkrm1 | TÇGCAAAGAT | TCTTCTGCAT | GTCACATTTA | AATCTCATCG 1262 |
| hkrm1 | TÄGCAAAGÄT | ACTTCTGCAC | GTCACATTCA | AATCCCATCG 1262 |
| mkrm2 | TCTGCTGGOT | CCAGGAAAAG | GTCTCTCTGGC | CATGGGGACCT 1221 |
| hkrm2 | TCTGCTGGCT | CCGGGAAAAG | GCCCCCGGC | GCRGGGGGGGT 1263 |
| mkrm1 hkrm1 mkrm2 hkrm2 | AGTCCCTGCA TGTTCCTGCT TCCCGGGCQ TCCAGGGC | TCAGGAGACC TCAGGGGACC CCGGGAGAAG CCMGGAGAAG | TTAGGGACTGTTAGGGGCTGTG | TCGTCAGCCT 1302 TCATCAACCA 1302 TGGTACCGCC 1261 TGGTACCAAC 1303 |
| mkrm1 | GGGGCTTCTG | GAGATATOTG | GACGATTTTC | TATGAACCTT 1342 TACAAGCCTT 1342 CAGGGGACTC 1301 CCGGGGACCC 1343 |
| hkrm1 | GGGACTTCGG | GGGAAATOTG | GAGCATTTTT | |
| mkrm2 | GGCCCCGAGG | GHIGGGGGTG | CCCTGTCCCC | |
| hkrm2 | AGCCCCAGG | GTGGCCTTG | CCCTGCTCCC | |
| mkrm1 | CCA. CTACA CCA. CTTCA TCAGGCTGAG CCAGGCTGAG | ATCTCCATCT | TTAAGAAGAA | GCTCAAGGGT 1380 |
| hkrm1 | | ATTTCCATCT | TTAAGAAGAA | ACTCAAGGGT 1380 |
| mkrm2 | | GGTGCTGCTG | CGGGCTACCG | TCCCCTGAGT 1341 |
| hkrm2 | | GGTTCTGCCG | CGGGCTACCG | GCCTCTGAGT 1383 |
| mkrm1 | CAGAGTCAAC | AAGATGACCG | CAATCCCTTCCAATCCCTTTGCGCTCGCTC | GTGAGTGACT 1420 |
| hkrm1 | CAGAGTCAAC | AAGATGACCG | | GTGAGTGACT 1420 |
| mkrm2 | GCCTCCAGCC | AGAGCTCCTT | | GTCTCTGCTC 1381 |
| hkrm2 | GCCTCCAGCC | AGAGCTCCCT | | ATCTCCGCTC 1423 |
| mkrml hkrml mkrm2 hkrm2 | GA 1422 AA 1422 TCTGA 1386 TCTGA 1428 | | | |

Multiple-alignment of mouse and human kremen DNAs (3-3)

Fig. 1 c

| mkrm1 hkrm1 mkrm2 hkrm2 | 1 1 1 | MAPPAARLALLSAALTLAARPAPÖPRS.GPECFTANGADYRGTOSWTÄLOG MAPPAARLALLSAAALTLAARPAPÖPGI.GPECFTÄNGADYRGTONWTÄLOG MÖTPHLOGFLLLFPLLLR.LHGASAGSLHSPGLSECFOVNGADYRGHONYTGPRG MÖTOALOGFLFLLFLDLLORRGASAGSLHSPGLSECFOVNGADYRGHONRTGPRG |
|----------------------------------|--------------------------|--|
| mkrm1 | 5 2 | .GEPCLFWNETFOHPYNETKYPNGEGGLGEHNYCRNPDGDVSPWCYVAEHEDGYY |
| hkrm1 | 5 2 | .GEPCLFWNETFOHPYNTLKYPNGEGGLGEHNYCRNPDGDVSPWCYVAEHEGYY |
| mkrm2 | 5 5 | AGRPCLFWDOTOOHSYSSASDPOGRWGLGAHNECRNPDGDVOPWCYVAETEEGIY |
| hkrm2 | 5 6 | AGRPCLFWDOTOOHSYSSASDPHGRWGLGAHNECRNPDGDVOPWCYVAETEEGIY |
| mkrm1 hkrm1 mkrm2 hkrm2 | 106 106 110 111 | MEACDIABGE WAGAPECEANDS GEBAPPT PER BERKT AGACETE CERRES ARE RECEINED OF THE CONTRACT OF C |
| mkrm1 | 161 | MESGYACFCGNNPDYWEIGEAASTECNSWCFGDHTOPCGGDGREILLEDTLVGACG |
| hkrm1 | 161 | WESGYACFCGNNPDYWEYGEAASTECNSWCFGDHTOPCGGDGREILLEDTLVGACG |
| mkrm2 | 165 | WEAGYACFCGSESDLARGREAPATDCDQICFGHEGOLCGGDGREGYWEVSVGSCQ |
| hkrm2 | 166 | WEAGYACFCGSESDLARGRUAPATDCDQFCFGEPGOLCGGDGREGYWEVSVGSCQ |
| mkrm1 | 216 | GNYSAMANVYSPDFPDTYATGRVCYWTERVPGASHEHFNFTLFDTRDSADMYEL |
| bkrm1 | 216 | GNYSAMSSVYYSPDFPDTYATGRVCYWTERVPGASHTHFSPLLFDTRDSADMYEL |
| mkrm2 | 220 | GNYSAMSSVYYSPDFPDEYGPDRNCSWVLGOLGAV. YELTFRLFETADSRDRDEL |
| bkrm2 | 221 | GNYTAPOGVTYSPDFPDEYGPDRNCSWALGPPGAA. HELTFRLFETADPRDRDEL |
| mkrm1 | 271 | LDGYTHRÜDVRLSGRSRPP.LSPNÜSLDFÜTLYFFSDRINQAQGFAÜLVQATKES |
| hkrm1 | 271 | LDGYTHRÜLARFHGRSRPP.LSPNÜSLDFÄTLYFFSDRINQAQGFAÜLVQATKES |
| mkrm2 | 274 | RDVSBGNÜLRAFDGAHPPPPGPLRÜRTAATÜLTPRSDARGHAQGFALTYRĞDQDT |
| hkrm2 | 275 | RDAASGSÜLRAFDGARPPPSGPLREGTAATÜLTFRSDARGHAQGFALTYRGLQDA |
| mkrm1 | 325 | PPQERPAVNOTIJAEVITEQANLSVSKAHSSKVLYVI PPSPSHPPQTAPGSHSWAP |
| hkrm1 | 325 | TPQERPAVNOTVAEVITEQANLSVSKARSSKVLYVIGTSPSHPPQTVPGSNSWAP |
| mkrm2 | 329 | VE. GRASPEDSTESLAGDPDGAN. ASCSP. PG. AA |
| hkrm2 | 330 | AB. DPEAPEGSAQTPAAPKDGAN. VSCSP. RPG. AP |
| mkrm1 hkrm1 mkrm2 hkrm2 | 380 380 361 362 | SVGANSKRVEGWTVYGLATILELTVTAKVAKLILHVT. FKSHRVEASG. EMGAGSKRVEGWTVYGLATILELTVTAKAKILLHVT. FKSHRVEASG. QASIGAKVFSTVTAKKULLLELSULREGAKRS |
| mkrm1 | 427 | .DLRDCROPGASGRIWTE PERSTTEST PKKKLKGOSOQDDRNPLVSD ~~~~ |
| hkrm1 | 427 | DLRDCHOPGTSGE IWST PYRPSTETST PKKKLKGOSOQDDRNPLVSD ~~~~~ |
| mkrm2 | 403 | LAMGPSRGPGRSWAWWYRPRGWALPCPPGDSOAEGPAAGYRPLSASSOSSL |
| hkrm2 | 417 | PALGASRGPRSWAWWYQOPRGWALPCSPGDPOAEGSAAGYRPLSASSOSSL |
| mkrm1 hkrm1 mkrm2 hkrm2 | 474 474 455 469 | RSLUSAL RSLUSAL |

Multiple-alignment of mouse and human Kremen proteins

Fig. 2

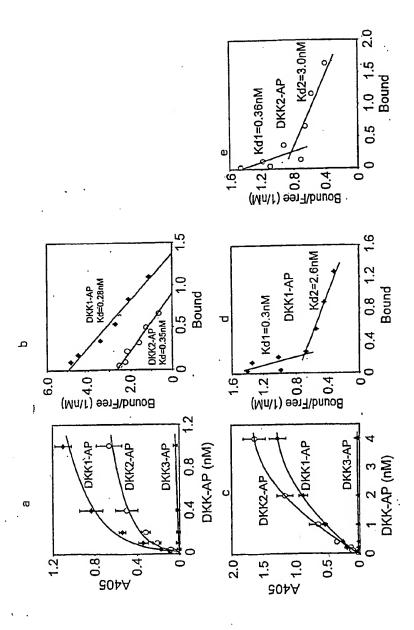


Fig. 3

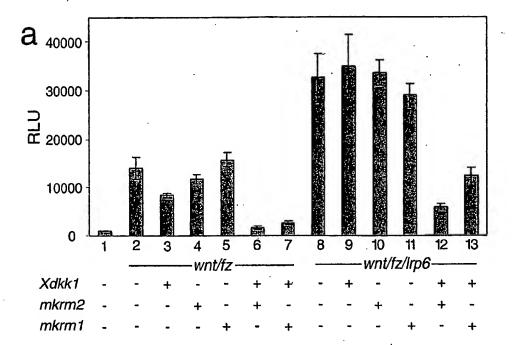


Fig. 4

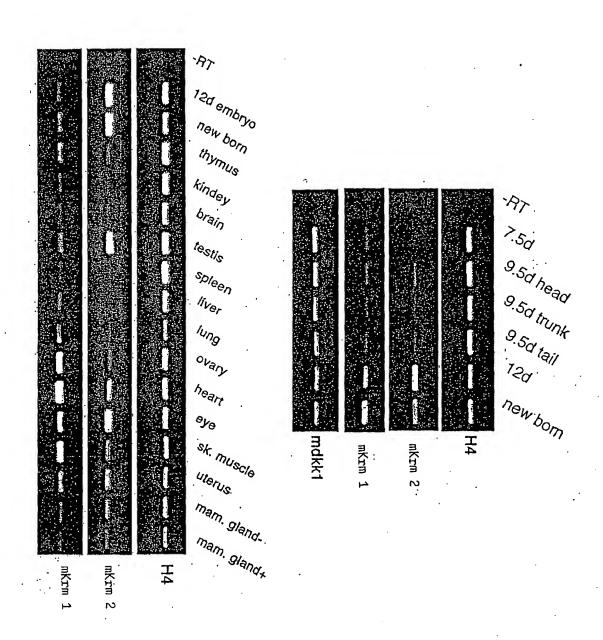


Fig. 5